

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/182,183ADATE: 09/29/94  
TIME: 14:27:03

INPUT SET: S354.raw

This Raw Listing contains the General  
Information Section and those Sequences  
containing ERRORS.

## SEQUENCE LISTING

## (1) General Information

- (i) APPLICANT: Lin et al.
- (ii) TITLE OF INVENTION: Glial Derived Neurotrophic Factor
- (iii) NUMBER OF SEQUENCES: 24
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Beaton & Swanson, P.C.
- (B) STREET: 4582 South Ulster Street Parkway, Suite #403
- (C) CITY: Denver
- (D) STATE: Colorado
- (E) COUNTRY: USA
- (F) ZIP: 80237
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
- (B) COMPUTER: IBM compatible
- (C) OPERATING SYSTEM: MS DOS
- (D) SOFTWARE: Wordperfect 5.1
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/182,183
- (B) FILING DATE: 5-MAY-1994
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/788,423, 07/774,109, 07/764,685
- (B) FILING DATE: 06-NOV-1991, 08-OCT-1991, 20-SEP-1991
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Barry J. Swanson
- (B) REGISTRATION NUMBER: 33,215
- (C) REFERENCE/DOCKET NUMBER: SYNE-225C<sup>4</sup>
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (303) 850-9900
- (B) TELEFAX: (303) 850-9401

→  
fix nucleic  
numbering

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/182,183ADATE: 09/29/94  
TIME: 14:27:06

INPUT SET: S354.raw

## ERRORED SEQUENCES FOLLOW:

78 (2) INFORMATION FOR SEQ ID NO:3  
79  
80 (i) SEQUENCE CHARACTERISTICS:  
--> 81 (A) LENGTH: 900 base pairs  
82 (B) TYPE: nucleic acid  
83 (C) STRANDEDNESS: single  
84 (D) TOPOLOGY: linear  
85  
86 (ix) FEATURE:  
87 (A) NAME/KEY: nucleic acid for rat GDNF  
88  
89 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
90  
91 CCCCCGGGCT GCAGGAATTC GGGG GTC TAC GGA GAC CGG ATC CGA GGT GCC  
--> 92 GCC  
93 Val Tyr Gly Asp Arg Ile Arg Gly Ala  
94 Ala  
95 -90 -85  
96  
97 GCC GGA CGG GAC TCT AAC ATG AAG TTA TGG GAT GTC GTG GCT GTC TGC 102  
98 Ala Gly Arg Asp Ser Lys Met Lys Leu Trp Asp Val Val Ala Val Cys  
99 -80 -75 -70  
100  
101 CTG GTG TTG CTG CAC ACC GCG TCT GCC TTC CCG CTG CCC GCC GGT AAG 150  
102 Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys  
103 -65 -60 -55  
104  
105 AGG CTT CTC GAA GCG CCC GCC GAA GAC CAC TCC CTC GGC CAC CGC CGC 198  
106 Arg Leu Leu Glu Ala Pro Ala Glu Asp His Ser Leu Gly His Arg Arg  
107 -50 -45 -40  
108  
109 GTG CCC TTC GCG CTG ACC AGT GAC TCC AAT ATG CCC GAA GAT TAT CCT 246  
110 Val Pro Phe Ala Leu Thr Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro  
111 -35 -30 -25 -20  
112  
--> 113 GAC CAG TTT GAT GAC GTC ATG GAT TTT ATT CAA GCC ACC ATC AAA AGA  
114 Asp Gln Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys Arg  
115 -15 -10 -5  
116  
--> 117 CTG AAA AGG TCA CCA GAT AAA CAA GCG GCG GCA CTT CCT CGA AGA GAG  
118 Leu Lys Arg Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu  
119 1 5 10  
120  
121 AGG AAC CGG CAA GCT GCA GCT GCC AGC CCA GAG AAT TCC AGA GGG AAA 390  
122 Arg Asn Arg Gln Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys  
123 15 20 25  
124

insert

S1  
54

296 294

342 OK

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/182,183A

 DATE: 09/29/94  
 TIME: 14:27:09

INPUT SET: S354.raw

125	GGT CGC AGA GGC CAG AGG GGC AAA AAT CGG GGG TGC GTC TTA ACT GCA	438
126	Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala	
127	30 35 40 45	
128		
129	ATA CAC TTA AAT GTC ACT GAC TTG GGT TTG GGC TAC GAA ACC AAG GAG	486
130	Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu	
131	50 55 60	
132		
133	GAA CTG ATC TTT CGA TAT TGT AGC GGT TCC TGT GAA GCG GCC GAG ACA	534
134	Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr	
135	65 70 75	
136		
137	ATG TAC GAC AAA ATACTA AAA AAT CTG TCT CGA AGT AGA AGG CTA ACA	582
138	Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr	
139	80 85 90	
140		
141	AGT GAC AAG GTA GGC CAG GCA TGT TGC AGG CCG GTC GCC TTC GAC GAC	630
142	Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp	
143	95 100 105	
144		
145	GAC CTG TCG TTT TTA GAC GAC AGC CTG GTT TAC CAT ATC CTA AGA AAG	678
146	Asp Leu Ser Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg Lys	
147	110 115 120 125	
148		
149	CAT TCC GCT AAA CGG TGT GGA TGT ATC TGA CCCTGGCTCC AGAGACTGCT	728
150	His Ser Ala Lys Arg Cys Gly Cys Ile	
151	130	
152		
153	GTGTATTGCA TTCCTGCTAC ACTGCGAAGA AAGGGACCAA GGTTCCCAGG	778
154	AAATATTTGC	788
155		
156	CCAGAAAGGA AGATAAGGAC CAAGAAGGCA GAGGCAGAGG CGGAAGAAGA	838
157	AGAAGAAAAG	848
158		
159	AAGGACGAAG GCAGCCATCT GTGGGAGCCT GTAGAAGGAG GCCCAGCTAC AG	900
160		
161		

 insert a nucleic acid on  
 each line

316	(2) INFORMATION FOR SEQ ID NO:8	
317		
318	(i) SEQUENCE CHARACTERISTICS:	
319	(A) LENGTH: 223 base pairs	
320	(B) TYPE: nucleic acid	
321	(C) STRANDEDNESS: single	
322	(D) TOPOLOGY: linear	
323		
324	(ix) FEATURE:	
325	(A) NAME/KEY: nucleic acid sequence for human GDNF	
326		
327	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
328		
329	TTCTCTCCCC CACCTCCCGC CTGCCC GCGC A GGT GCC GCC GCC GGA CGG GAC	
330	TTT	55

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/182,183A

DATE: 09/29/94  
TIME: 14:27:13

INPUT SET: S354.raw

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331                                     Gly Ala Ala Ala Gly Arg Asp
332 Phe
333                                     -5
334
335 AAG ATG AAG TTA TGG GAT GTC GTG GCT GTC TGC CTG GTG CTG CTC CAC      103
336 Lys Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His
337      1              5              10              15
338
339 ACC GCG TCC GCC TTC CCG CTG CCC GCC GGT AAG AGG CCT CCC GAG GCG      151
340 Thr Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala
341              20              25              30
342
343 CCC GCC GAA GAC CGC TCC CTC GGC CGC CGC CGC GCG CCC TTC GCG CTG      199
344 Pro Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu
345              35              40              45
346
347 AGC AGT GAC TGTAAGAACC GTTCC      223
348 Ser Ser Asp
349      50
350

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/182,183A**DATE: 09/29/94  
TIME: 14:27:14**INPUT SET: S354.raw**

Line	Error	Original Text
81	Entered (900) and Calc. Seq. Length (749) differ	(A) LENGTH: 900 base pairs
92	# of Sequences for line conflicts w/ running total	GCC
113	# of Sequences for line conflicts w/ running total	GAC CAG TTT GAT GAC GTC ATG GAT TTT ATT CA
117	# of Sequences for line conflicts w/ running total	CTG AAA AGG TCA CCA GAT AAA CAA GCG GCG G
154	# of Sequences for line conflicts w/ running total	AAATATTTGC
157	# of Sequences for line conflicts w/ running total	AGAAGAAAAG
319	Entered (223) and Calc. Seq. Length (171) differ	(A) LENGTH: 223 base pairs
330	# of Sequences for line conflicts w/ running total	TTT